

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/386,680DATE: 11/26/95
TIME: 17:52:45

INPUT SET: S14073.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/386,680
(B) FILING DATE: 10-FEB-1995
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/167,628
(B) FILING DATE:(A) APPLICATION NUMBER: US/07/752,427
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100
(B) TELEFAX: 619-455-5110

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47

48 (2) INFORMATION FOR SEQ ID NO:1:

49

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2075 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

55

56 (ii) MOLECULE TYPE: cDNA

57

58

59 (vii) IMMEDIATE SOURCE:

60 (B) CLONE: DB60R32

61

62 (ix) FEATURE:

63 (A) NAME/KEY: CDS

64 (B) LOCATION: 130..1177

65

66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68

69 CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG 60

70

71 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA 120

72

73 GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC 168

74 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe

75 1 5 10

76

77 GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC 216

78 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys

79 15 20 25

80

81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG 264

82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala

83 30 35 40 45

84

85 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC 312

86 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala

87 50 55 60

88

89 AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC 360

90 Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His

91 65 70 75

92

93 AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC 408

94 Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly

95 80 85 90

96

97 GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG 456

98 Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val

99 95 100 105

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100																		
101	TAC	CGC	AGC	GGA	GAG	TCC	TTC	CAG	AGC	AGC	TGC	AAG	TAC	CAG	TGC	ACG		504
102	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr		
103	110					115					120					125		
104																		
105	TGC	CTG	GAC	GGG	GCG	GTG	GGC	TGC	ATG	CCC	CTG	TGC	AGC	ATG	GAC	GTT		552
106	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val		
107					130					135						140		
108																		
109	CGT	CTG	CCC	AGC	CCT	GAC	TGC	CCC	TTC	CCG	AGG	AGG	GTC	AAG	CTG	CCC		600
110	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro		
111				145					150					155				
112																		
113	GGG	AAA	TGC	TGC	GAG	GAG	TGG	GTG	TGT	GAC	GAG	CCC	AAG	GAC	CAA	ACC		648
114	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr		
115			160					165					170					
116																		
117	GTG	GTT	GGG	CCT	GCC	CTC	GCG	GCT	TAC	CGA	CTG	GAA	GAC	ACG	TTT	GGC		696
118	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly		
119		175					180					185						
120																		
121	CCA	GAC	CCA	ACT	ATG	ATT	AGA	GCC	AAC	TGC	CTG	GTC	CAG	ACC	ACA	GAG		744
122	Pro	Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu		
123	190					195					200					205		
124																		
125	TGG	AGC	GCC	TGT	TCC	AAG	ACC	TGT	GGG	ATG	GGC	ATC	TCC	ACC	CGG	GTT		792
126	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val		
127					210					215					220			
128																		
129	ACC	AAT	GAC	AAC	GCC	TCC	TGC	AGG	CTA	GAG	AAG	CAG	AGC	CGC	CTG	TGC		840
130	Thr	Asn	Asp	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys		
131				225				230						235				
132																		
133	ATG	GTC	AGG	CCT	TGC	GAA	GCT	GAC	CTG	GAA	GAG	AAC	ATT	AAG	AAG	GGC		888
134	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly		
135			240				245						250					
136																		
137	AAA	AAG	TGC	ATC	CGT	ACT	CCC	AAA	ATC	TCC	AAG	CCT	ATC	AAG	TTT	GAG		936
138	Lys	Lys	Cys	Ile	Arg	Thr	Pro											

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153 ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT 1128
154 Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn
155 320 325 330
156
157 GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T 1177
158 Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
159 335 340 345
160
161 GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACTGA TTCACATCTC 1237
162
163 ATTTTTCCTG AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG 1297
164
165 GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC 1357
166
167 CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC 1417
168
169 CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT 1477
170
171 CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA 1537
172
173 AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC 1597
174
175 CAGCCATCAA GAGACTGAGT CAAGTTGTTT CTTAAGTCAG AACAGCAGAC TCAGCTCTGA 1657
176
177 CATTCTGATT CGAATGACAC TGTTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT 1717
178
179 TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAATATTT 1777
180
181 GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA 1837
182
183 AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA 1897
184
185 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957
186
187 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA 2017
188
189 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCAGC 2075
190
191

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

203 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
204 1 5 10 15
205

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206	Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
207				20					25					30		
208																
209	Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
210			35					40					45			
211																
212	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
213		50					55					60				
214																
215	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
216	65					70					75					80
217																
218	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr
219					85					90					95	
220																
221	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser
222				100					105						110	
223																
224	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
225			115					120					125			
226																
227	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro
228		130					135					140				
229																
230	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys
231	145					150					155					160
232																
233	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly
234					165					170					175	
235																
236	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro
237				180					185					190		
238																
239	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala
240			195					200					205			
241																
242	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp
243		210					215					220				
244																
245	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg
246	225					230					235					240
247																
248	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys
249					245					250					255	
250																
251	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly
252				260					265					270		
253																
254	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr
255			275					280					285			
256																
257	Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu
258		290					295						300			

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SEQUENCE VERIFICATION REPORT
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Original Text